II. AMENDMENT

Please amend the claims as follows:

(Claims 1-45, Canceled)

46. (Previously Amended) A method comprising:
   a) contacting one or more species of yeast in a sample with one or more yeast specific enzyme-linked probes, under suitable *in-situ* hybridization conditions, to thereby form one or more probe/target sequence hybrids within the yeast; and
   b) detecting enzyme activity within the yeast to thereby determine the presence, absence, identity or number of yeast in the sample.

47. (Previously Amended) The method of claim 46 further comprising:
   c) isolating the yeast using a filter as an isolation medium.

48. (Previously Amended) The method of claim 47, further comprising:
   d) growing the isolated yeast by culture in media.

49. (Previously Amended) The method of claim 48, wherein the culture is grown directly on the filter, under suitable culture conditions, by placing the filter in contact with media.

(Claims 50-60, Canceled)

61. (Previously Amended) A method for detecting, identifying or quantitating *Dekkera/Brettanomyces* yeast in a sample; said method comprising:
   a) contacting one or more species of yeast in the sample with one or more *Dekkera/Brettanomyces* yeast specific probes, under suitable hybridization conditions, to thereby form a probe/target sequence hybrid; and

b) detecting the presence, absence or amount of probe/target sequence hybrid and correlating the result with the presence, absence or number of *Dekkera/Brettanomyces* yeast in the sample;

wherein one or more of the *Dekkera/Brettanomyces* yeast specific probes comprise a probing nucleobase sequence wherein at least a portion of the probing nucleobase sequence is at least ninety percent homologous to the nucleobase sequences selected from the group consisting of: AGC-GGG-TCT-ATT-AGA (Seq. ID No. 1); CCA-GGT-GAG-GGT-CGC (Seq. ID No. 2); CGG-TTG-CCC-GAT-TTC (Seq. ID No. 3); TCG-CCT-TCC-TCC-TCT (Seq. ID No. 4); CGG-TCT-CCA-GCG-ATT (Seq. ID No. 5); CAC-AAG-ATG-TCC-GCG (Seq. ID No. 6); GCG-GGC-ACT-AAT-TGA (Seq. ID No. 7); CAT-CCA-CGA-GGA-ACG (Seq. ID No. 8); GTG-TAA-ACC-AGG-TGC (Seq. ID No. 9); ATG-GCT-CCC-AGA-ACC (Seq. ID No. 10) and GAC-AGA-ATC-GAA-GGG (Seq. ID No. 11) and sequences fully complementary thereto and of the same length.

62. (Previously Amended) The method of claim 61, wherein the probing nucleobase sequences of said one or more probes are selected to be one hundred percent homologous to a nucleobase sequence identified in the claim.

(Claims 63-82, Canceled)

83. (Previously Amended) A method comprising:

a) filtering a fixed volume of a liquid sample comprising yeast using a filter having a pore size that does not allow the yeast to pass;

b) incubating the filter containing the yeast, in media and under culture conditions, for 45 or fewer hours to thereby grow microcolonies of the yeast;

c) fixing the microcolonies of the yeast to the filter;

d) contacting the microcolonies of the yeast with a yeast specific enzyme-linked probe, under suitable *in-situ* hybridization conditions, to thereby form one or more probe/target sequence hybrids within the yeast;

e) detecting enzyme activity within the yeast to thereby determine the presence, absence or number of yeast sought to be detected in the sample; and

f) determining the quantity of the yeast in the sample;

wherein the yeast are slow growing and the method is performed within 48 hours.

84. (Previously Amended) The method of claim 83, wherein fixing the microcolonies of yeast to the filter and contacting the microcolonies of yeast with a yeast specific enzyme-linked probe are performed simultaneously using a single solution.

85. (Previously Amended) The method of claim 83, wherein the number of CFU in the sample is determined.

(Claims 86-87, Canceled)

88. (Previously Presented) The method of claim 49, wherein colonies grown on the filter represent the number of colony forming units (CFU) present in the sample.

89. (Previously Presented) The method of claim 48, wherein the yeast are slow growing yeast.

90. (Previously Presented) The method of claim 89, wherein the identity and number of slow growing yeast in the culture is determined within 48 hours.

91. (Previously Presented) The method of claim 46, wherein the target sequence is ribosomal RNA.

92. (Previously Presented) The method of claim 91, wherein the ribosomal RNA target sequence is specific for detecting *Dekkera/Brettanomyces* yeast in the sample.

93. (Previously Presented) The method of claim 91, wherein the ribosomal RNA target sequence is specific for detecting *Dekkera bruxellensis* yeast in the sample.

94. (Previously Presented) The method of claim 46, wherein the one or more yeast specific enzyme-linked probes are selected to detect a particular species of yeast.

95. (Previously Presented) The method of claim 46, wherein the one or more yeast specific enzyme-linked probes are selected to detect members of a genus of a yeast.

96. (Previously Presented) The method of claim 46, wherein the one or more yeast specific enzyme-linked probes are selected to detect all yeast present in the sample.

97. (Previously Presented) The method of claim 46, wherein the enzyme-linked probe is an enzyme-linked peptide nucleic acid probe.

98. (Previously Presented) The method of claim 97, wherein the probe is a soy bean peroxidase labeled peptide nucleic acid probe.

(Claims 99-104, Canceled)